22Sept99

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0157153 DBA Accession No.: 93-15205 PATENT

**Detection of point** mutation **using** mismatch **repair enzyme- by hybridization of DNA probe and binding of enzyme or DNA cleavage, for use in genetic disease diagnosis**

PATENT ASSIGNEE: Univ.Maryland 1993

PATENT NUMBER: WO 9320233 PATENT DATE: 931014 WPI ACCESSION NO.: 93-336939 (9342)

PRIORITY APPLIC. NO.: US 859072 APPLIC. DATE: 920327

NATIONAL APPLIC. NO.: WO 93US2329 APPLIC. DATE: 930322

LANGUAGE: English

ABSTRACT: A new method for identifying a point mutation site in a nucleic acid comprises: obtaining single-stranded target nucleic acid; **hybridizing** oligonucleotides containing the site to the single-stranded nucleic acid, where the oligonucleotides may or may not be complementary at the site, to form a hybrid; exposing the hybrids to a mismatch repair enzyme which binds to mismatch bases to form an enzyme-nucleic acid complex, or that cleaves 1 strand containing a mismatched base pair; determining the presence of complexes or cleaved fragments; and identifying the base at the site. The enzyme may bind to or cleave at AG or TG base pairs, and the DNA may be **labeled** with a radiolabel, enzyme or dye, with cleaved fragments differentially **labeled** . A set of 2 primer pairs, of which 1 of each pair **hybridizes** the point mutation sequence and the other does not, is claimed. The method is useful in genetic disease diagnosis. (43pp)

DESCRIPTORS: point mutation det. method, DNA probe hybridization, mismatch repair enzyme binding or DNA cleavage, appl. genetic disease diagnosis (Vol.12, No.26)

SECTION: PHARMACEUTICALS-Clinical Genetic Techniques; GENETIC ENGINEERING AND FERMENTATION-Nucleic Acid Technology (D7,A1)

0180691 DBA Accession No. 95-08711 PATENT

**Immobilized mismatch-binding protein for detection or purification of mutations or polymorphisms - mutS immobilization and application**

AUTHOR: Wagner Jr R E
PATENT ASSIGNEE: Gene-Check 1995

PATENT NUMBER: WO 9512689 PATENT DATE: 950511 WPI ACCESSION NO.: 95-185788 (9524)
PRIORITY APPLIC. NO.: US 147785 APPLIC. DATE: 931104
NATIONAL APPLIC. NO.: WO 94US12768 APPLIC. DATE: 941104
LANGUAGE: English

ABSTRACT: A new method for detecting a mutation from a non-mutated sequence of a target DNA in a sample involves: incubating a chromogenic-, chemiluminescent-, bioluminescent-, fluorescent-or biotin-labeled or radiolabeled polynucleotide or oligonucleotide from the sample with a mismatch-binding protein (I) immobilized on a solid surface (especially a nitrocellulose membrane) under conditions favoring binding of the mismatch-containing polynucleotides and immobilized (I); and detecting binding, where the presence of the labeled polynucleotides or oligonucleotides is indicative of a mutation in the sequence of the target DNA. (I) is the MutS protein or a derivative. Also new are: a method for detecting a mutation from a non-mutated sequence of mammalian ds target DNA; a method for removal from amplified DNA sample of minority sequences and sequence errors introduced during the amplification; a method for identifying a specific allele in a multi-allelic system in a sample of amplified DNA; a kit useful for the detection of a mutation from a non-mutated sequence of a target polynucleotide sequence in a sample; and immobilized (I). (39pp)

DESCRIPTORS: DNA polymorphism analysis, purification, **point mutation detection** , immobilized mutS **mismatch** -binding **protein** immobilization (Vol.14, No.15)
SECTION: GENETIC ENGINEERING AND FERMENTATION-Nucleic Acid Technology (A1)

0158109 DBA Accession No. 94-00660 PATENT

**Genetic screening for nucleotide variation- point mutation detection by hybridization, polymerase chain reaction and mismatch binding protein affinity chromatography**

PATENT ASSIGNEE: Massachusetts-Inst.Technol. 1993

PATENT NUMBER: WO 9322457 PATENT DATE: 931111 WPI ACCESSION NO.: 93-368815 (9346)

PRIORITY APPLIC. NO.: US 874192 APPLIC. DATE: 920424

NATIONAL APPLIC. NO.: WO 93US3777 APPLIC. DATE: 930422

LANGUAGE: English

ABSTRACT: A new method for genetic screening for nucleotide variation comprises: subjecting target and reference nucleic acids to conditions which allow them to anneal and produce a heteroduplex, each containing a mismatched nucleotide pair; treating the mixture with a mismatch binding protein, to bind this protein to the pair; and detecting the presence of the mismatch. The mismatch binding protein may be used as an adsorbent in affinity adsorption. The nucleic acid may first be amplified by the polymerase chain reaction, and the heteroduplex may also contain polymerase chain reaction tails. The heteroduplex may be labeled. Detection may also involve formation of an immune complex between an antibody and either the bound mismatch binding protein or the bound heteroduplex. The method has greatly increased sensitivity, and does not rely on restriction fragment length differences. The method also allows enrichment of heteroduplex fragments containing mismatches, even in samples containing excess homoduplex, allowing more sensitive detection of the mismatch. (88pp)

DESCRIPTORS: point mutation det. method, hybridization, polymerase chain reaction, mismatch binding protein affinity chromatography DNA amplification (Vol.13, No.2)

SECTION: GENETIC ENGINEERING AND FERMENTATION-Nucleic Acid Technology (A1)

?ds

| Set | Items | Description |
|---|---|---|
| S1 | 16 | (MUTATION(3N)MISMATCH?) AND (HYBRIDIZ?(S)LABEL?) |
| S2 | 11 | RD (unique items) |
| S3 | 0 | (POINT()MUTATION()DETECTION)(S)(MUT S) |
| S4 | 3 | (POINT()MUTATION()DETECTION)(S)(MISMATCH(3N)PROTEIN) |

2/5/9 (Item 6 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
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0146445 DBA Accession No.: 93-04497 PATENT
**Method for detection of** mismatch mutation **in DNA- rapid and simple method for disease diagnosis or cancer diagnosis**
PATENT ASSIGNEE: Upstate-Biotechnol. 1993
PATENT NUMBER: WO 9302216 PATENT DATE: 930204 WPI ACCESSION NO.: 93-058809 (9307)
PRIORITY APPLIC. NO.: US 732219 APPLIC. DATE: 910719
NATIONAL APPLIC. NO.: WO 92US6045 APPLIC. DATE: 920717
LANGUAGE: English
ABSTRACT: A new rapid, efficient and cheap method for detecting a mutation in a single-stranded polynucleotide (ssP) in a biological sample comprises: incubating the sample with an ssP **hybridization** partner (HP) comprising at least 1 ss base sequence complementary to the non-mutated sequence of the target polynucleotide, under conditions suitable for **hybridization** of the HP to any mutated or non-mutated sequences of the target polynucleotide to form a hybrid; contacting the hybrid with a mismatch-binding protein (MBP) (MutS protein, a derivative or a MutS-beta-galactosidase (BGal, EC-3.2.1.23) fusion protein (FP)); and detecting MBP bound to the hybrid (by addition of a **labeled** 1st binding partner, especially an antibody, capable of binding to the MBP or by addition of an unlabeled 1st binding partner and a **labeled** 2nd binding partner (antibody, MutL protein, MutL derivative, MutL-BGal-FP or enzyme) and detecting the 2nd). The HP is DNA or cDNA which is immobilized on a solid surface (nitrocellulose membrane). The target polynucleotide is DNA, and it is subjected to enzymic restriction prior to denaturation. A kit for the new method is also claimed. (76pp)
E.C. NUMBERS: 3.2.1.23
DESCRIPTORS: point mutation, deletion, addition, detection method, DNA probe hybridization, mismatch-binding protein, appl. disease, cancer diagnosis MutS MutL beta-galactosidase fusion protein enzyme antibody EC-3.2.1.23 tumor
SECTION: PHARMACEUTICALS-Clinical Genetic Techniques; GENETIC ENGINEERING AND FERMENTATION-Nucleic Acid Technology (D7,A1)

0208116 DBA Accession No. 97-03237 PATENT

**Use of nucleic acid repair enzyme- diagnostic method for point mutation detection by oligonucleotide DNA probe hybridization and cleavage product detection**

AUTHOR: Chirikjian J G; Collier B G
CORPORATE SOURCE: Gaithersburg, MD, USA.
PATENT ASSIGNEE: Trevigen 1996
PATENT NUMBER: WO 9640902 PATENT DATE: 961219 WPI ACCESSION NO.: 97-099933 (9709)
PRIORITY APPLIC. NO.: US 12950 APPLIC. DATE: 960306
NATIONAL APPLIC. NO.: WO 96US8694 APPLIC. DATE: 960607
LANGUAGE: English
ABSTRACT: A new method for detection of a point mutation in a target DNA involves: stringent **hybridization** of an ss oligonucleotide (ON) DNA probe to form a hybrid ds DNA, with a **mismatch** at the point **mutation** site; cleaving the probe at a predetermined temp. with a nucleic acid repair enzyme (e.g. mutY, T/G-mismatch-specific nicking enzyme, human or yeast all-type enzyme or Escherichia coli deoxyinosine-3'-endonuclease), optionally combined with a DNA-lyase or a DNA-AP-endonuclease, to dissociate ON fragments spontaneously at this temp.; repeating these steps; and detecting the ON fragments to indicate the presence of the point mutation. Cleavage may be effected by a glycosylase attached to the probe and an AP cleaving enzyme. A 2nd and/or 3rd probe may be **hybridized** to the target at an adjacent location, with separate cleavage components attached, and optionally with different lengths and fluorescence **labels** . A repair index for a mismatched or damaged ON probe may be determined using this method. The method may be used in accurate and efficient genetic disease diagnosis, without DNA amplification. (66pp)
DESCRIPTORS: point mutation det. method, oligonucleotide DNA probe **hybridization** , mismatch DNA repair enzyme cleavage, fluorescence **label** , appl. diagnostic mutY nicking enzyme human yeast all-type enzyme Escherichia coli deoxyinosine-3'-endonuclease glycosylase DNA-lyase DNA-AP-endonuclease DNA sequence protein sequence (Vol.16, No.6)
SECTION: PHARMACEUTICALS-Clinical Genetic Techniques; GENETIC ENGINEERING AND FERMENTATION-Nucleic Acid Technology (D7,A1)

23 Sept 99

>>SET HILIGHT: use ON, O[redacted] or 1-5 characters
6018 PNA
25257 POINT MUTATION
242463 HYBRIDIZ?
S1 8 PNA AND (POINT MUTATION)AND HYBRIDIZ?
?rd
...completed examining records
S2 6 RD (unique items)
?t s2/5/all

**2/5/1 (Item 1 from file: 73)**
DIALOG(R)File 73:EMBASE
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07446764 EMBASE No: 1998357080
PNA **array technology in molecular diagnostics**
Geiger A.; Lester A.; Kleiber J.; Orum H.
H. Orum, PNA Diagnostics A/S, Ronnegade 2, DK-2100 Copenhagen O Denmark
Nucleosides and Nucleotides ( NUCLEOSIDES NUCLEOTIDES ) (United States) 1998, 17/9-11 (1717-1724)

CODEN: NUNUD ISSN: 0732-8311
DOCUMENT TYPE: Journal; Conference Paper
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 17

A comparative study using immobilised DNA and **PNA** oligomers demonstrates the suitability of **PNA** molecules as sequence specific capture probes in the detection of single point mutations in a DNA analyte and in the analysis of complex analyte mixtures.

DRUG DESCRIPTORS:
*peptide nucleic acid
oligomer; dna
MEDICAL DESCRIPTORS:
*molecular mimicry; *nucleic acid **hybridization**
dna probe; nucleotide sequence; immobilization; luminescence; **point mutation** ; conference paper

CAS REGISTRY NO.: 9007-49-2 (dna)

SECTION HEADINGS:
029 Clinical and Experimental Biochemistry

**2/5/2 (Item 2 from file: 73)**
DIALOG(R)File 73:EMBASE
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07130081 EMBASE No: 1998015073
**Genetic analysis by peptide nucleic acid affinity MALDI-TOF mass spectrometry**
Griffin T.J.; Tang W.; Smith L.M.
L.M. Smith, Department of Chemistry, University of Wisconsin-Madison, 1101 University Ave., Madison, WI 53706-1396 United States
AUTHOR EMAIL: smith@chem.wisc.edu
Nature Biotechnology ( NAT. BIOTECHNOL. ) (United States) 1997, 15/13 (1368-1372)

CODEN: NABIF ISSN: 1087-0156
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 24

The ability to analyze multiple polymorphic sites rapidly and accurately is crucial in all areas of genetic analysis. We have developed an approach for the detection of multiple point mutations, using allele-specific, mass-labeled, peptide nucleic acid (**PNA** ) **hybridization** probes, and direct

analysis by matrix-assis[redacted] laser desorption/ionization t[redacted]-of-flight mass spectrometry. The composite mass spectra produced contain peaks of distinct masses corresponding to each allele present, resulting in a mass spectral 'fingerprint' for each DNA sample. The **hybridization** characteristics of **PNA** :DNA duplexes were found to be highly dependent on both base content and sequence. Results from the analysis of four polymorphic sites contained in exon 4 of the human tyrosinase gene show that this approach is simple, rapid, and accurate with potential applications in many areas of genetic analysis.

DRUG DESCRIPTORS:
*peptide; *nucleic acid
dna; monophenol monooxygenase

MEDICAL DESCRIPTORS:
*genetic analysis; *nucleic acid **hybridization** ; *mass spectrometry
protein nucleic acid interaction; dna fingerprinting; **point mutation** ;
exon; genome; dna polymorphism; human; article; priority journal

CAS REGISTRY NO.: 9007-49-2 (dna); 9002-10-2 (monophenol monooxygenase)

SECTION HEADINGS:
022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation

**2/5/3 (Item 3 from file: 73)**
DIALOG(R)File 73:EMBASE
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06890886 EMBASE No: 1997175265
**Detection of point mutation in the p53 gene using peptide nucleic acid biosensor**
Wang J.; Rivas G.; Cai X.; Chicharro M.; Parrado C.; Dontha N.; Begleiter A.; Mowat M.; Palecek E.; Nielsen P.E.
J. Wang, Dept. of Chemistry and Biochemistry, New Mexico State University, Las Cruces, NM 88003 United States
Analytica Chimica Acta ( ANAL. CHIM. ACTA ) (Netherlands) 1997, 344/1-2 (111-118)

CODEN: ACACA ISSN: 0003-2670
PUBLISHER ITEM IDENTIFIER: S0003267097000391
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 14

A 17-mer peptide nucleic acid (**PNA** ) is used as the recognition layer of an electrochemical biosensor for detecting a specific mutation in the p53 gene. The performance of the **PNA** -derived biosensor is compared with that of its DNA counterpart. The significantly higher specificity of the **PNA** probe greatly improves the detection of a single point mutation, found in many types of cancer. Factors influencing the surface immobilization of the **PNA** probe, its **hybridization** to the p53 target sequence, and the chronopotentiometric detection step, are explored and optimized. This and similar developments hold promise for the diagnosis and management of cancer.

DRUG DESCRIPTORS:
*protein p53--endogenous compound--ec
peptide nucleic acid

MEDICAL DESCRIPTORS:
*electrochemistry; *genetic analysis
article; biosensor; cancer--diagnosis--di; cancer--etiology--et; human; nonhuman; **point mutation** ; priority journal; technique

SECTION HEADINGS:
016 Cancer

022 Human Genetics
029 Clinical and Experimental Biochemistry

**2/5/4 (Item 4 from file: 73)**
DIALOG(R)File 73:EMBASE
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06220694 EMBASE No: 1995257098
**Enhanced PCR amplification of VNTR locus D1S80 using peptide nucleic acid ( PNA)**
Demers D.B.; Curry E.T.; Egholm M.; Sozer A.C.
Fairfax Identity Laboratories, Genetics and IVF Institute, 3025 Hamaker Ct,Ste 203 Fairfax, VA 22031 United States
Nucleic Acids Research ( NUCLEIC ACIDS RES. ) (United Kingdom) 1995, 23/15 (3050-3055)

CODEN: NARHA ISSN: 0305-1048
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Use of the polymerase chain reaction (PCR) to amplify variable numbers of tandem repeat (VNTR) loci has become widely used in genetic typing. Unfortunately, preferential amplification of sinall allelic products relative to large allelic products may result in incorrect or ambiguous typing in a heterozygous sample. The mechanism for preferential amplification has not been elucidated. Recently, **PNA** oligomers (peptide nucleic acids) have been used to detect single base mutations through PCR clamping. **PNA** is a DNA mimic that exhibits several unique **hybridization** characteristics. In this report we present a new application of **PNA** which exploits its unique properties to provide enhanced amplification. Rather than clamping the PCR, **PNA** is used to block the template making it unavailable for interstrand and intrastrand interactions while allowing polymerase to displace the **PNA** molecules and extend the primer to completion. Preferential amplification is reduced and overall efficiency is enhanced.

DRUG DESCRIPTORS:
oligomer; peptide nucleic acid

MEDICAL DESCRIPTORS:
*gene amplification; *polymerase chain reaction
allele; article; consensus sequence; controlled study; dna determination; dna template; gene locus; gene technology; human; human cell; **point mutation** ; priority journal; tandem repeat

SECTION HEADINGS:
021 Developmental Biology and Teratology
022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical and Experimental Biochemistry

**2/5/5 (Item 1 from file: 144)**
DIALOG(R)File 144:Pascal
(c) 1999 INIST/CNRS. All rts. reserv.

13356195 PASCAL No.: 98-0083742
**Mismatch-sensitive** hybridization **detection by peptide nucleic acids immobilized on a quartz crystal microbalance**
WANG J; NIELSEN P E; JIANG M; CAI X; FERNANDES J R; GRANT D H; OZSOZ M; BEGLIETER A; MOWAT M
Department of Chemistry and Biochemistry, New Mexico State University, Las Cruces, New Mexico 88003, United States; Center for Biomolecular Recognition, IMBG, Department of Biochemistry B, The Panum Institute, Blegdamsvej 3c, 2200, Copenhagen, Denmark; Manitoba Institute of Cell Biology, Winnipeg, Manitoba R5E OV9, Canada
Journal: Analytical chemistry : (Washington, DC), 1997, 69 (24)

5200-5202
ISSN: 0003-2700 CODEN: ANCHAM Availability: INIST-120B; 354000079772680390
No. of Refs.: 16 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: United States
Language: English

A quartz crystal microbalance DNA **hybridization** biosensor, based on thiol-derivatized peptide nucleic acid (**PNA** ) probes, offers unusual in situ differentiation of single-base mismatches. A large excess of a single-base mismatch oligonucleotide has no effect on the frequency response of the target Such remarkable distinction between perfect matches and mismatches is illustrated by the detection of a common mutation in the p53 gene. The greater specificity of the new mass-sensitive indicatorless **hybridization** device over those of analogous **PNA** -based carbon electrodes is attributed to the formation of a **PNA** monolayer and the use of a hydrophilic ethylene glycol linker. The improved specificity is coupled to very fast (3-5 min) **hybridization** in a low-ionic-strength medium.

English Descriptors: **Point mutation** ; Base mismatching; Investigation method; Molecular probe; Molecular hybrid; Peptides; Nucleic acid; Immobilization; Quartz microbalance; Biosensor; Tumor suppressor gene

French Descriptors: Mutation ponctuelle; Mesappariement base; Methode etude ; Sonde moleculaire; Hybride moleculaire; Peptide; Acide nucleique; Immobilisation; Microbalance quartz; Biodetecteur; Gene suppresseur tumeur; Gene p53

Classification Codes: 002A31C09B; 215
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**2/5/6 (Item 1 from file: 155)**
DIALOG(R)File 155:MEDLINE(R)
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09607880 98324861
**Detection of the hereditary hemochromatosis gene mutation by real-time fluorescence polymerase chain reaction and peptide nucleic acid clamping.**
Kyger EM; Krevolin MD; Powell MJ
Roche Diagnostics Boehringer-Mannheim Corporation, 4300 Hacienda Drive, Pleasanton, California, 94588-2722, USA. erich kyger@mgc.boehringer-mannheim.com
Anal Biochem (UNITED STATES) Jul 1 1998, 260 (2) p142-8, ISSN 0003-2697 Journal Code: 4NK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
JOURNAL ANNOUNCEMENT: 9810
Subfile: INDEX MEDICUS

Hereditary hemochromatosis (HH), an iron overload disease, is the most common known inheritable disease. The most prevalent form of HH is believed to be the result of a single base-pair mutation. We describe a rapid homogeneous mutation analysis method that does not require post-polymerase chain reaction (PCR) manipulations. This method is a marriage of three emerging technologies: rapid cycling PCR thermal cyclers, peptide nucleic acid ( **PNA** ) probes, and a new double-stranded DNA-selective fluorescent dye, Sybr Green I. The LightCycler is a rapid thermal cycler that fluorometrically monitors real-time formation of amplicon with Sybr Green I. PNAs are DNA mimics that are more sensitive to mismatches than DNA probes, and will not serve as primers for DNA polymerases. **PNA** probes were designed to compete with PCR primers **hybridizing** to the HH mutation site. Fully complemented **PNA** probes at an 18:1 ratio over DNA primers with a mismatch result in suppression of amplicon formation. Conversely, **PNA** probes with a mismatch will not impair the binding of a complementary primer, culminating in amplicon formation. A LightCycler-based rapid genetic assay has been developed to distinguish HH patients from HH

carriers and normal individuals using **PNA** clamping technology. Copyright 1998 Academic Press.

Tags: Human

Descriptors: Hemochromatosis--Genetics--GE; *Oligodeoxyribonucleotides; * **Point Mutation** ; Base Composition; Base Sequence; DNA Primers; Fluorescent Dyes; Genetic Techniques; Heterozygote Detection; Homozygote; Oligonucleotide Probes; Peptides; Polymerase Chain Reaction--Methods--MT; Spectrometry, Fluorescence--Methods--MT

CAS Registry No.: 0 (DNA Primers); 0 (Fluorescent Dyes); 0 (Oligodeoxyribonucleotides); 0 (Oligonucleotide Probes); 0 (Peptides); 163795-75-3 (SYBR Green I)

3 July 2000

| Set | Items | Description |
|---|---|---|
| S1 | 24019 | (GREEN()FLUORESCENT()PROTEIN) OR GFP |
| S2 | 4408752 | S1 AND MISMATCH OR C/C |
| S3 | 46 | S1 AND MISMATCH |
| S4 | 18 | RD (unique items) |
| S5 | 2 | S4 AND (C/C) |
| S6 | 171 | S2 AND MISMATCH (2N)BINDING |
| S7 | 71 | RD (unique items) |
| S8 | 70 | S7 AND (C/C) |
| S9 | 0 | S8 AND GFP(2N)LABE |
| S10 | 0 | S8 AND GFP (2N) LABEL |
| S11 | 0 | S8 AND GFP (4N) LABELED |
| S12 | 3 | S8 AND MISMATCHED (2N) BASE? |
| S13 | 49 | S8 NOT PY>=1999 |
| S14 | 49 | RD (unique items) |
| S15 | 19868 | S1 AND (GREEN()FLUORESCENT()PROTEIN) |
| S16 | 1 | S1 AND (MISMATCH (2N) BINDING) |
| S17 | 532 | AU="HAYASHIZAKI Y" OR AU="HAYASHIZAKI Y." OR AU="HAYASHIZA-KI YOSHIHIDE" |
| S18 | 161 | RD (unique items) |
| S19 | 1 | S18 AND (GREEN()FLUORESCENT()PROTEIN OR GFP) |
| S20 | 114 | S1 AND (PROTEIN()LABEL?) |
| S21 | 35 | RD (unique items) |

11211658 BIOSIS NO.: 199799832803
Construction of a %green% fluorescent %protein% %labeled% gE mutant of HSV for studies of intercellular viral spread.
AUTHOR: Chin M S(a); Margolis T P; Mendoza N T; Lavail J H
AUTHOR ADDRESS: (a)Dep. Anatomy, UCSF, San Francisco, CA 94143**USA
1997
JOURNAL: Society for Neuroscience Abstracts 23 (1-2):p2197 1997
CONFERENCE/MEETING: 27th Annual Meeting of the Society for Neuroscience New Orleans, Louisiana, USA October 25-30, 1997
ISSN: 0190-5295
RECORD TYPE: Citation
LANGUAGE: English
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Infection; Nervous System (Neural Coordination); Sense Organs (Sensory Reception)
BIOSYSTEMATIC NAMES: Herpesviridae--Viruses
ORGANISMS: herpes simplex virus type-1 (Herpesviridae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): microorganisms; viruses
MISCELLANEOUS TERMS: Meeting Abstract; Meeting Poster; CELL-TO-CELL VIRAL SPREAD; CORNEAL EPITHELIAL CELLS; %GREEN% %FLUORESCENT% %PROTEIN% ; INFECTION; INFECTIOUS BLINDNESS; NERVOUS SYSTEM; PATHOGEN; SENSORY SYSTEM; TRIGEMINAL NERVE ENDINGS; VIRAL GLYCOPROTEIN E; VIRAL REACTIVATION
CONCEPT CODES:
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10068 Biochemical Studies-Carbohydrates
20006 Sense Organs, Associated Structures and Functions-Pathology
20504 Nervous System-Physiology and Biochemistry
20506 Nervous System-Pathology
36006 Medical and Clinical Microbiology-Virology
00520 General Biology-Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals
BIOSYSTEMATIC CODES: